

SEQUENCE LISTING

T3007
(1) GENERAL INFORMATION:

(i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,

5 (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
... (D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 92037

15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 30-AUG-1991
(C) CLASSIFICATION:

25 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wecherell, Jr. Ph.D., John W.
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-1294

30 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-455-5100
(B) TELEFAX: 619-455-5110

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
(B) TYPE: nucleic acid
5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DB60R32

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
... (B) LOCATION: 130..1177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCGGCCGAC	AGCCCCGAGA	CGACAGCCCG	GCGCGTCCCG	GTCCCCACCT	CCGACCACCG	60	
15	CCAGGGCTCC	AGGCCCGCG	CTCCCCGCTC	GCGGCCACCG	CGCCCTCCGC	TCCGGCCCGCA	120
	GTGCCAACCC	ATG ACC GCC	GCC AGT ATG	GGC CCC GTC	CGC GTC	GCC TTC	168
	Met Thr Ala	Ala Ser Met	Gly Pro Val	Arg Val Ala	Phe		
	1	5	10				
20	GTG GTC CTC	CTC GCC CTC	TGC AGC CCG	CCG GCC GTC	GGC CAG AAC	TGC	216
	Val Val Leu	Leu Ala	Leu Cys Ser	Arg Pro Ala	Val Gly Gln	Asn Cys	
	15	20	25				
	AGC GGG CCG	TGC CGG TGC	CCG CCG GAC	GAG CCG GCG	CCG CGC TGC	CCG GCG	264
	Ser Gly Pro	Cys Arg Cys	Pro Asp Glu	Pro Pro Ala	Arg Cys Pro	Ala	
	30	35	40	45			
25	GGC GTG AGC	CTC GTG CTG	GAC GGC TGC	GGC TGC TGC	CGC GTC	TGC GCC	312
	Gly Val Ser	Leu Val Leu	Asp Gly Cys	Gly Cys Cys	Arg Val Cys	Ala	
	50	55	60				
30	AAG CAG CTG	GGC GAG CTG	TGC ACC GAG	CGC GAC CCC	TGC GAC CCG	CAC	360
	Lys Gln Leu	Gly Glu Leu	Cys Thr	Glu Arg Asp	Pro Cys Asp	Pro His	
	65	70	75				

	AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC	408
	Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly	
	80 85 90	
5	GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG	456
	Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val	
	95 100 105	
	TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG	504
	Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr	
	110 115 120 125	
10	TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT	552
	Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val	
	130 135 140	
15	CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC	600
	Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro	
	145 150 155	
	GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC	648
	Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr	
	160 165 170	
20	GTG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC	696
	Val Val Gly Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe Gly	
	175 180 185	
	CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG	744
	Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu	
	190 195 200 205	
25	TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT	792
	Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val	
	210 215 220	
	ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC	840
	Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys	
30	225 230 235	
	ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC	888
	Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly	
	240 245 250	

	AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG	936
	Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu	
	255 260 265	
5	CIT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA	984
	Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly	
	270 275 280 285	
	GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG	1032
	Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu	
	290 295 300	
10	CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG	1080
	Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met	
	305 310 315	
15	ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT	1128
	Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn	
	320 325 330	
	GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T	1177
	Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala	
	335 340 345	
20	GAAGCCAGAG AGTGAGAGAC ATTAACATCAT TAGACTGGAA CTTGAACATGA TTACACATCTC	1237
	ATTTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG	1297
	GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC	1357
	CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGAA ACTACATTAG TACACAGCAC	1417
	CAGAATGTAT ATTAAGGTGT GGCTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT	1477
	CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAAT TGAGAAGGAA	1537
25	AATTTTAGGG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC	1597
	CAGCCATCAA GAGACTGAGT CAAGTTGTTG CTTAAGTCAG AACAGCAGAC TCAGCTCTGA	1657
	CATTCTGATT CGAATGACAC TGTTCAAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT	1717
	TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTA AAATTTATAT TGTAAATATT	1777
	GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA	1837

AGTTGTTTGT GCCTTTAT TTTGTTTT AATGCTTG AATTCAATG TTAGCCTCAA 1897
TTCTGAACA CCATAGGTAG AATGTAAGC TTGCTGATC GTTCAAAGCA TGAAATGGAT 1957
ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCGT CAAAACAGAT TGTGGAAA 2017
GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG 2075

5 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
1 5 10 15

Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
15 20 25 30

Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Arg Val Cys Ala Lys Gln Leu
50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
20 65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
25 100 105 110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115 120 125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
130 135 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
145 150 155 160

5 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
165 170 175

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
180 185 190

10 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
195 200 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
210 215 220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
225 230 235 240

15 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
245 250 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
260 265 270

20 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
275 280 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu
290 295 300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
305 310 315 320

25 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
325 330 335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
340 345

35